

Sequences producing significant alignments:			Score (bits)	E Value
gi 55642389 ref XP_523094.1	PREDICTED: similar to Presenil...	452	e-126	
gi 37182518 gb AAQ89061.1	TAAV688 [Homo sapiens]	451	e-125	G
gi 50726954 ref NP_112591.2	presenilin stabilization facto...	449	e-125	G
gi 12052866 emb CAB66606.1	hypothetical protein [Homo sapi...	447	e-124	G
gi 55726744 emb CAH90134.1	hypothetical protein [Pongo pyg...	444	e-123	
gi 29243936 ref NP_808251.1	hypothetical protein 4632417K0...	391	e-107	G
gi 34864291 ref XP_217185.2	similar to RIKEN cDNA 0610008A...	377	e-103	G
gi 21492616 ref NP_080950.1	RIKEN cDNA 0610008A10 [Mus mus...	369	e-101	G
gi 37682171 gb AAQ98012.1	anterior pharynx defective 1B-li...	284	2e-75	G
gi 34864287 ref XP_343418.1	similar to RIKEN cDNA 0610008A...	282	7e-75	G
gi 17389295 gb AAH17699.1	APH-1A protein [Homo sapiens] >g...	256	7e-67	G
gi 15990414 gb AAH15568.1	APH-1A protein [Homo sapiens] >g...	254	2e-66	G
gi 12654775 gb AAH01230.1	APH-1A protein [Homo sapiens]	254	2e-66	G
gi 56268871 gb AAH87081.1	Unknown (protein for MGC:94545) ...	253	5e-66	
gi 22203751 ref NP_666216.1	anterior pharynx defective 1A ...	252	8e-66	G
gi 34858248 ref XP_345252.1	similar to Aph1a-pending prote...	252	1e-65	G
gi 18848275 gb AAH24111.1	6530402N02Rik protein [Mus muscu...	251	2e-65	G

gi 7705787 ref NP_057106.1	CGI-78 protein [Homo sapiens] >...	248	2e-64	G
gi 26324468 dbj BAC25988.1	unnamed protein product [Mus mu...	246	6e-64	G
gi 47214485 emb CAG12490.1	unnamed protein product [Tetrao...	211	3e-53	
gi 48095709 ref XP_392345.1	similar to CG2855-PA [Apis mel...	178	1e-43	G
gi 54644318 gb EAL33059.1	GA15487-PA [Drosophila pseudoobs...	172	1e-41	
gi 20129183 ref NP_608710.1	CG2855-PA [Drosophila melanoga...	164	3e-39	G
gi 55236032 gb EAA14158.3	ENSANGP00000015809 [Anopheles ga...	164	4e-39	
gi 26347159 dbj BAC37228.1	unnamed protein product [Mus mu...	162	1e-38	G
gi 31233667 ref XP_318923.1	ENSANGP00000015809 [Anopheles ...	158	2e-37	G
gi 50806123 ref XP_428797.1	PREDICTED: similar to Anterior...	154	3e-36	G
gi 56204871 emb CAI22813.1	likely ortholog of C. elegans a...	145	1e-33	
gi 50809568 ref XP_429030.1	PREDICTED: similar to anterior...	121	3e-26	G
gi 39580694 emb CAE70374.1	Hypothetical protein CBG16933 [...	81	4e-14	
gi 17509423 ref NP_492469.1	i-78 protein like, Anterior PH...	74	7e-12	G
gi 50252282 dbj BAD28287.1	presenilin stabilization factor...	71	3e-11	
gi 20453379 gb AAM19928.1	At2g31440/T28P16.7 [Arabidopsis ...	70	6e-11	G
gi 21594204 gb AAM65980.1	unknown [Arabidopsis thaliana]	69	1e-10	
gi 56500904 emb CAH94855.1	conserved hypothetical protein ...	37	0.90	
gi 22024126 ref NP_610786.2	CG8545-PA [Drosophila melanoga...	36	1.5	G
gi 32403290 ref XP_322258.1	hypothetical protein [Neurospo...	35	2.0	G
gi 9837379 gb AAG00551.1	retinitis pigmentosa GTPase regul...	35	2.0	
gi 31621286 tpg DAA01153.1	TPA: RT11 [Mus musculus] >gi 46...	35	2.6	G
gi 2209198 gb AAB61441.1	LOX6 [Helobdella robusta]	35	2.6	
gi 32414609 ref XP_327784.1	hypothetical protein [Neurospo...	35	3.4	G
gi 55588200 ref XP_513809.1	PREDICTED: hypothetical protei...	35	3.4	
gi 51458782 ref XP_371313.2	PREDICTED: similar to dJ14N1.2...	35	3.4	G
gi 12314268 emb CAC13173.1	novel S-100\ICaBP type calcium...	35	3.4	
gi 32423411 ref XP_332143.1	predicted protein [Neurospora ...	34	4.5	G
gi 53719504 ref YP_108490.1	putative lipoprotein [Burkhold...	34	4.5	G
gi 53723509 ref YP_102951.1	TPR domain protein [Burkholder...	34	4.5	G
gi 42554029 gb EAA76872.1	hypothetical protein FG07524.1 [...	34	5.8	G
gi 46444603 gb EAL03877.1	hypothetical protein CaO19.1574 ...	34	5.8	
gi 46444453 gb EAL03728.1	hypothetical protein CaO19.9147 ...	34	5.8	
gi 56315671 emb CAI10315.1	hypothetical protein [Azoarcus ...	34	5.8	
gi 46228566 gb EAK89436.1	hypothetical protein with possib...	34	5.8	
gi 7488765 pir T10863	extensin precursor - kidney bean >gi...	23	7.0	
gi 41054255 ref NP_956076.1	nuclear autoantigenic sperm pr...	33	7.6	G
gi 51557560 ref YP_068394.1	putative ORF-3 protein [Suid h...	33	7.6	G
gi 22328344 ref NP_680595.1	hypothetical protein [Arabidop...	33	7.6	G
gi 32563629 ref NP_491994.2	chromo domain and SNF2 related...	33	9.9	G
gi 23508533 ref NP_701202.1	hypothetical protein [Plasmodi...	33	9.9	G
gi 55741482 ref NP_055840.1	myelin transcription factor 1-...	33	9.9	G
gi 51708299 ref XP_143396.3	PREDICTED: similar to dJ14N1.2...	33	9.9	G
gi 50418016 gb AAH77951.1	Irx2-A protein [Xenopus laevis]	33	9.9	G
gi 7504867 pir T23056	hypothetical protein H06001.2 - Caen...	33	9.9	
gi 9837383 gb AAG00553.1	retinitis pigmentosa GTPase regul...	33	9.9	

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|55642389|ref|XP_523094.1| PREDICTED: similar to Presenilin stabilization fac
troglodytes]
Length = 389

Score = 452 bits (1162), Expect = e-126
Identities = 231/259 (89%), Positives = 231/259 (89%)
Frame = +3

Query: 3 VAMTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARV 182
VAMTAAVFFGCAFIAGFPALALYVFTIA EPLRIIFLIAGA MARV
Sbjct: 131 VAMTAAVFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARV 190

Query: 183 IIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAY 362
IIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAY
Sbjct: 191 IIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAY 250

Query: 363 VSGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFF 542
VSGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFF
Sbjct: 251 VSGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFF 310

Query: 543 DGCEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSL 722
DGCEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSL
Sbjct: 311 DGCEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSL 370

Query: 723 KLCLLCQDKNFLLYNQRSR 779
KLCLLCQDKNFLLYNQRSR
Sbjct: 371 KLCLLCQDKNFLLYNQRSR 389

☐ >gi|37182518|gb|AAQ89061.1| ☒ TAAV688 [Homo sapiens]
Length = 257

Score = 451 bits (1159), Expect = e-125
Identities = 230/257 (89%), Positives = 230/257 (89%)
Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGA MARVII
Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS
Sbjct: 61 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFFDG 548
GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFFDG
Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL
Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
CLLCQDKNFLLYNQRSR
Sbjct: 241 CLLCQDKNFLLYNQRSR 257

>gi|50726954|ref|NP_112591.2| [G] presenilin stabilization factor-like [Homo sapiens]
 gi|18088649|gb|AAH20905.1| [G] Presenilin stabilization factor-like [Homo sapiens]
 Length = 257

Score = 449 bits (1154), Expect = e-125
 Identities = 229/257 (89%), Positives = 229/257 (89%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGFPALALYVFTIA EPLRIIFLIAGA MARVII
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 368
 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS
 Sbjct: 61 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 548
 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
 CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL
 Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
 CLLCQDKNFLLYNQRSR
 Sbjct: 241 CLLCQDKNFLLYNQRSR 257

>gi|12052866|emb|CAB66606.1| [G] hypothetical protein [Homo sapiens]
 gi|37077447|sp|Q8WW43|AP1B_HUMAN [G] Gamma-secretase subunit APH-1B (APH-1b) (Aph-1
 stabilization factor-like)
 gi|24637564|gb|AAN63817.1| [G] presenilin stabilization factor-like protein [Homo sapiens]
 Length = 257

Score = 447 bits (1150), Expect = e-124
 Identities = 228/257 (88%), Positives = 229/257 (89%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGFPALALYVFTIA EPLRIIFLIAGA MARVII
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 368
 DNKDGPTQKYLLIFGAFVSVYI+EMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS
 Sbjct: 61 DNKDGPTQKYLLIFGAFVSVYIREMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 548
 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
 CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL
 Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
 CLLCQDKNFLLYNQRSR
 Sbjct: 241 CLLCQDKNFLLYNQRSR 257

>gi|55726744|emb|CAH90134.1| hypothetical protein [Pongo pygmaeus]
 Length = 257

Score = 444 bits (1142), Expect = e-123
 Identities = 226/257 (87%), Positives = 228/257 (88%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGFPALALYVFTIA EPLRIIFLIAGA MARVII
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DNKDGPTQKYLLIFG FVSVYIQEMFRFAYY+LLKKASEGLKSINPGETAPSMRLLAYVS
 Sbjct: 61 DNKDGPTQKYLLIFGTFFSVYIQEMFRFAYYRLKKASEGLKSINPGETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 548
 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKL 728
 CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKL
 Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
 CLLCQDK+FLLYNQRSR
 Sbjct: 241 CLLCQDKDFLLYNQRSR 257

>gi|29243936|ref|NP_808251.1| [G] hypothetical protein 4632417K02 [Mus musculus]
 gi|50927492|gb|AAH79659.1| [G] Hypothetical protein 4632417K02 [Mus musculus]
 gi|26340556|dbj|BAC33940.1| [G] unnamed protein product [Mus musculus]
 gi|37077156|sp|Q8C7N7|AP1B_MOUSE [G] Gamma-secretase subunit APH-1B
 Length = 257

Score = 391 bits (1004), Expect = e-107
 Identities = 194/257 (75%), Positives = 210/257 (81%)
 Frame = +3



Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGFPALALYVFTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DN+DGP Q YLLIFG +SV IQE+FR AYYKLLKKASEGLKSINP ETAPSMRLLAYVS
 Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYKLLKKASEGLKSINPEETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 548
 GLGFGIMSGVFSFVNTLS+SLGPGTVGIHGDSPQFFL SAFMTLV+I+LHVFVG+VFFDG
 Sbjct: 121 GLGFGIMSGVFSFVNTLSNSLPGPTVGIHGDSPQFFLNSAFMTLVVIMLHVFVGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLKL 728
 CEK KW S QTF+S YY +NL +A+II+VLMG WAF AGGSCRSLKL
 Sbjct: 181 CEKNKWYTLTLLTVLLTHLVSTQTFLSPYYEVNLVTAYIIMVLMGIWAFYVAGGSCRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
 CLLCQDK+FLLYNQRSR
 Sbjct: 241 CLLCQDKDFLLYNQRSR 257

 >gi|34864291|ref|XP_217185.2|  similar to RIKEN cDNA 0610008A10 [Rattus norvegicus]
 Length = 257

Score = 377 bits (968), Expect = e-103
 Identities = 189/257 (73%), Positives = 207/257 (80%)
 Frame = +3






Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGXXXXXXXXXXXXXXXXXMARVII 188
 MTA VFFGCAFIAGFPALALY+FTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTAPVFFGCAFIAGFPALALYLFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DN+DGP Q YLLIFG +SV IQE+FR AYY+LLKKASEGLKSINP ETAPSMRLLAYVS
 Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKASEGLKSINPEETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFVGIVFFDG 548
 GLGFGIMSGVFSFVNTLS++LPGTVGIHGDSPQFFL SAFMTLVII+LHVFVGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSFVNTLSNALPGTVGIHGDSPQFFLNSAFMTLVIIIMLHVFVGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLKL 728
 CEK KW S QT +S +Y +NL +A+II+VLMG WAF AGGS RSLKL
 Sbjct: 181 CEKNKWYILLTVLLTHLLVSTQTLLSPHYEVNLVTAYIIMVLMGIWAFVAGGSRRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
 CLLCQDK+FLLYNQRSR
 Sbjct: 241 CLLCQDKDFLLYNQRSR 257

 >gi|21492616|ref|NP_080950.1|  RIKEN cDNA 0610008A10 [Mus musculus]
 gi|38648719|gb|AAH63254.1|  RIKEN cDNA 0610008A10 [Mus musculus]
 gi|29747906|gb|AAH50923.1|  RIKEN cDNA 0610008A10 [Mus musculus]
 gi|37077773|sp|Q9DCZ9|AP1C MOUSE Putative gamma-secretase subunit APH-1C
 gi|12832198|dbj|BAB22004.1|  unnamed protein product [Mus musculus]
 Length = 258

Score = 369 bits (948), Expect = e-101
 Identities = 186/258 (72%), Positives = 204/258 (79%), Gaps = 1/258 (0%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGXXXXXXXXXXXXXXXXXMARVII 188
 MT VFFGCAFIAGFPA ALY+FTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTLPVFFGCAFIAGFPAFALYLFTIATDPLRVIFLIAGAFFWLVSLLLSSMFVFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGET-APSMRLLAYV 365
 +N+D Q YLLIFGA +SV IQE+FR AYYKLLKKASEGLKSINP E APSMRLLAYV
 Sbjct: 61 NNRDESQVQNYLLIFGALLSVCIQELFRLAYYKLLKKASEGLKSINPEEDIAPSMRLLAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLGPCTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFFD 545
 SGLGFGIMSGVFSFVNTLS+SLGPCTVGIHGDSPOFFL SAFMTLV+I+LHVFWG+VFFD
 Sbjct: 121 SGLGFGIMSGVFSFVNTLSNSLGPCTVGIHGDSPOFFLNSAFMTLVVIMLHVFWGVVFFD 180

Query: 546 GCEKKKKGXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSK 725
 GCEK KW S QTF+S YY +NL +A+II+VLMG WAF AGGSCRSK
 Sbjct: 181 GCEKNKWYTLTLTVLLTHLVVSTQTFSPYYEVNLTAYIIMVLMGIWAFYVAGGSCRSK 240

Query: 726 LCLLCQDKNFLLYNQSR 779
 CLLCQDK+FLLYNQSR
 Sbjct: 241 FCLLCQDKDFLLYNQSR 258

>gi|37682171|gb|AAQ98012.1| [G] anterior pharynx defective 1B-like [Danio rerio]
 gi|41056229|ref|NP_956409.1| [G] anterior pharynx defective 1B [Danio rerio]
 gi|22001127|gb|AAM88325.1| [G] Aph-1 protein [Danio rerio]
 gi|47939453|gb|AAH71492.1| [G] Anterior pharynx defective 1B [Danio rerio]
 gi|37077309|sp|Q8JHE9|AP1B_BRARE Gamma-secretase subunit Aph-1b (Anterior-pharynx
 1b)
 Length = 258

Score = 284 bits (726), Expect = 2e-75
 Identities = 147/259 (56%), Positives = 183/259 (70%), Gaps = 2/259 (0%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MT AVFFGC FIAFGPA+AL++FTIA +PLR+IFLIAGA + V I
 Sbjct: 1 MTVAVFFGCTFIAFGPAIALFMFTIARDPLRVIFLIAGAFFWLVSLLLSSLVWFIT-VQI 59

Query: 189 DNKDGPTQKY-LLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLAY 362
 NK+ TQ+ LLIFG +SV +QE FR+ YY+LLKKA+EGL +++ +T P SMR LAY
 Sbjct: 60 SNKNSATQQRGLLIFGVVLSVLLQEAFRYGYRLLKKANEGLLALSQEDTMPISMRQLAY 119

Query: 363 VSGLGFGIMSGVFSFVNTLSDSLGPCTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFF 542
 VSGLGFG MSG FS VN LSDSLGPCTVGIHG+S +F+ SAFMTL IILLH+FWG+VFF
 Sbjct: 120 VSGLGFGMSGAFSVVNILSDSLGPCTVGIHGESHYFISSAFMTLAIILLHMFVGIVFF 179

Query: 543 DGCEKKKKGXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSK 722
 + CE+++W S TF++ +Y +L +IIL +M WA+L AGGS R+L
 Sbjct: 180 EACERQRWWALGAVVASHLVVSLTFVNPYQGLIPTIYIILSVMVWAYLCAGGSLRNL 239

Query: 723 KLCLLCQDKNFLLYNQSR 779
 KLCL C+DK+FLL N R R
 Sbjct: 240 KLCLTCKDKDFLLANHRPR 258

>gi|34864287|ref|XP_343418.1| [G] similar to RIKEN cDNA 0610008A10 [Rattus norvegi]
 Length = 216

Score = 282 bits (722), Expect = 7e-75
 Identities = 151/257 (58%), Positives = 168/257 (65%)
 Frame = +3








Query: 9 MTAAVFFGCAFIAPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAPAL+LYVFTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTAAVFFGCAFIAPALSIVFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DN+DGP Q YLLIFG +SV IQE+FR AYY+LLKKA+EGLKSINP ETAPSMRLLAY
 Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKANEGGLKSINPEETAPSMRLLAY-- 118

Query: 369 GLGFGIMSGVFSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 548
 AFMTLVII+LHVFVGIVFFDG
 Sbjct: 119 -----AFMTLVIIIMLHVFVGIVFFDG 139

Query: 549 CEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAF LAAGGSCRS LKL 728
 CEK KW S QT +S +Y +NL +A+II+VLMG WAF AGGS RSLKL
 Sbjct: 140 CEKNKWYILLTVLLTHLLVSTQTLLSPHYEVNLVTAYIIMVLMGIWAF CVAGGSRRSLKL 199

Query: 729 CLLCQDKNFLLYNQ RSR 779
 CLLCQDK+FLLYNQ RSR
 Sbjct: 200 CLLCQDKDFLLYNQ RSR 216

 >gi|17389295|gb|AAH17699.1|  APH-1A protein [Homo sapiens]
 gi|14250557|gb|AAH08732.1|  APH-1A protein [Homo sapiens]
 gi|14550502|gb|AAH09501.1|  APH-1A protein [Homo sapiens]
 gi|37183020|gb|AAQ89310.1|  GAAV579 [Homo sapiens]
 gi|56204870|emb|CAI22812.1| likely ortholog of C. elegans anterior pharynx defect
 (APH-1A) [Homo sapiens]
 gi|25989508|gb|AAM61955.1|  presenilin stabilization factor a [Homo sapiens]
 gi|22761292|dbj|BAC11529.1|  unnamed protein product [Homo sapiens]
 Length = 247

Score = 256 bits (653), Expect = 7e-67
 Identities = 129/247 (52%), Positives = 166/247 (67%), Gaps = 1/247 (0%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 M AAVFFGC F+AFGPA AL++ T+A +PLR+I L+AGA + +
 Sbjct: 1 MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLLAYV 365
 D D Q LLIFGA VSV +QE+FRFAYYKLLKKA EGL S++ +P S+R +AYV
 Sbjct: 61 DRSDARLQYGLLIFGA AVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFD 545
 SGL FGI+SGVFS +N L+D+LGPG VGIHGDSP +FL SAF+T IILLH FWG+VFFD
 Sbjct: 121 SGLSFGIISGVFSVINILADALGPGVVG IGHGDSPYYFLTSAFLTAAILLHTFWGVVFFD 180

Query: 546 GCEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAF LAAGGSCRS LK 725
 CE++++ S TF++ +Y +L + + V MG WAF+ AGGS RS++
 Sbjct: 181 ACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQ 240

Query: 726 LCLLCQD 746
 LLC+D
 Sbjct: 241 RSL LCKD 247

 >gi|15990414|gb|AAH15568.1|  APH-1A protein [Homo sapiens]
 gi|18088501|gb|AAH20590.1|  APH-1A protein [Homo sapiens]